

OM of: US-09-823-373-5 to: GenEmbl.* out_format : pfs
Date: Sep 18, 2002 3:27 PM
About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL-frame1 p2n.model -DEV-xlh
-O/Cgnt2_1/USPTO.spool/US09823373/runat_17092002.085948.23516/app_query.fasta_1.431
-DB-GenEmbl -QFMT-fastap -SUFFIX-rge -GAPOP-12.000 -GAPEXT-4.000
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-XGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELET=7.000 -START=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
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-NCPU=6 -TCPUP=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:

y: US-09-823-373-5

y length: 369

Database: GenEmbl.*

Database sequences: 1797656

Database length: 187333701

Search time (sec): 1922.480000

score_list:

Sequence	Strd Orig	zScore	EScore	Len	Documentation
gb_ba:RERLAL	+	1363.00	2094.25	276-108	D12583 Rhodococcus rhodochrous
gb_ba:RERLAL	+	995.50	1527.96	9.6e-77	D11425 R. rhodochrous DNA for
gb_ba:RERLAL	+	995.50	1519.28	2.9e-76	D67026 Rhodococcus rhodochrous
gb_ba:RERLAL	+	994.50	1526.02	1.2e-76	E90026 DNA encoding nitrilase
gb_ba:RERLAL	+	992.50	1521.96	2.1e-76	AX235749 Sequence 1 from Patent
gb_ba:RERLAL	+	869.50	1333.64	6.4e-66	AX036235 Sequence 3 from Patent
gb_ba:RERLAL	+	869.50	1333.64	6.4e-66	E12616 DNA encoding novel nitr
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gb_ba:RERLAL	+	776.00	1190.56	5.9e-58	AX189646 Sequence 3 from Patent
gb_ba:RERLAL	+	696.50	1033.38	2.6e-50	AX028892 Bacillus sp. Oxb-1 on
gb_ba:RERLAL	+	676.00	1030.39	5.0e-49	AX008753 Sequence 2 from Patent
gb_ba:RERLAL	+	676.00	1030.39	5.0e-49	AX025996 Sequence 1 from Patent
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gb_ba:RERLAL	+	558.50	847.62	7.5e-39	AF130936 Fusarium solani chy
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gb_pl:ATNITA + 394.50 597.80 6.2e-25 1306 | X68305 A.thaliana mRNA for
gb_pl:ATNIT + 392.50 594.53 9.4e-25 1331 | X63445 A.thaliana mRNA for
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seq_name: gb_ba:RERLAL

seq_documentation_block:

LOCUS RERLAL 1653 bp DNA linear BCT 03-FEB-1999
DEFINITION Rhodococcus rhodochrous aliphatic nitrilase gene, complete cds.
ACCESSION D12583
VERSION D12583.1 GI:216931
KEYWORDS aliphatic nitrilase.
SOURCE Rhodococcus rhodochrous (strain:K22) DNA.
ORGANISM Rhodococcus rhodochrous
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Nocardiaceae; Nocardiaceae; Rhodococcus.
Kobayashi, M.
Direct Submission

REFERENCE 1 (bases 1 to 1653)
AUTHORS Kobayashi, M.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1992) Michihiko Kobayashi, Kyoto University,
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(Tel:075-753-6114, Fax:075-753-6128)

REFERENCE 2 (bases 1 to 1653)
AUTHORS Kobayashi, M., Yanaka, N., Nagasawa, T. and Yamada, H.
TITLE Primary structure of an aliphatic nitrile-degrading enzyme,
aliphatic nitrilase, from Rhodococcus rhodochrous K22 and
expression of its gene and identification of its active site
residue
JOURNAL Biochemistry 31 (37), 9000-9007 (1992)

MEDLINE 93003039
COMMENT Submitted (07-JUL-1992) to DDBJ by:
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Location/Qualifiers
1. .1653
/organism="Rhodococcus rhodochrous"
/strain="K22"
/db_xref="taxon:1829"
302. .307
314. .1465
/EC_number="3.5.5.1"
/codon_start=1
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/protein_id="BAA02127.1"
/db_xref="GI:216932"
/translation="MSSNPGLKYTKVAVVQAPVILDADATDKAIGTIEEAKN
GAELFAPEWIPGPYVWAWGVDVFKYHNSLTIGDDMRRLQAAHQNN
IALVNGYSEKDGASRYLSQVFDQNGDIVANRRKLKPTHTVITYEGNGDTFLTHDF
GFGVGGKNCWEHFQPLSKYMYSLNEQIHVSWPAMFALPDVHOLSVEANDVTRFS
VAIEGOTFLVASTHVIGATDLPAGDDAKRALPLGQWARIYGPQKSLAEPLPE
DAEGLYAELEDEQLILAKAAADPAGHSRDPVLSKIDTRNHTPVQYITADGRTSLN
SNSRVYRLHQLADIEKYENNEATLPDAPAPAPAEQSGRAKAA"

FEATURES

source

RBS

CDS

repeat_region

BASE COUNT 340 a 586 c 467 g 260 t
ORIGIN /rpt_type=Inverted

alignment_scores:

Quality: 1363.00 Length: 369
Ratio: 4.143 Gaps: 3
Percent Similarity: 89.160 Percent Identity: 71.274

